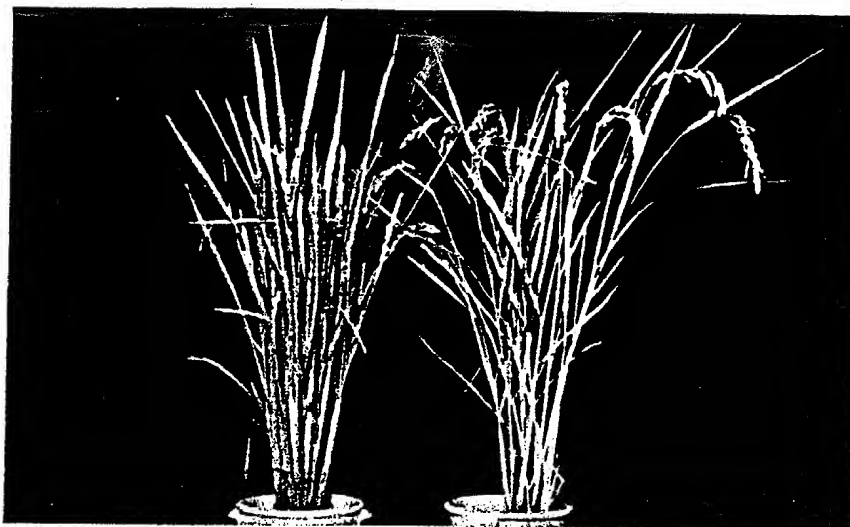


A

Mutant
(A0369 -/-)

Wild Type
(Akitakomachi)



B

Mutant
(A0369 -/-)

Wild Type
(Akitakomachi)

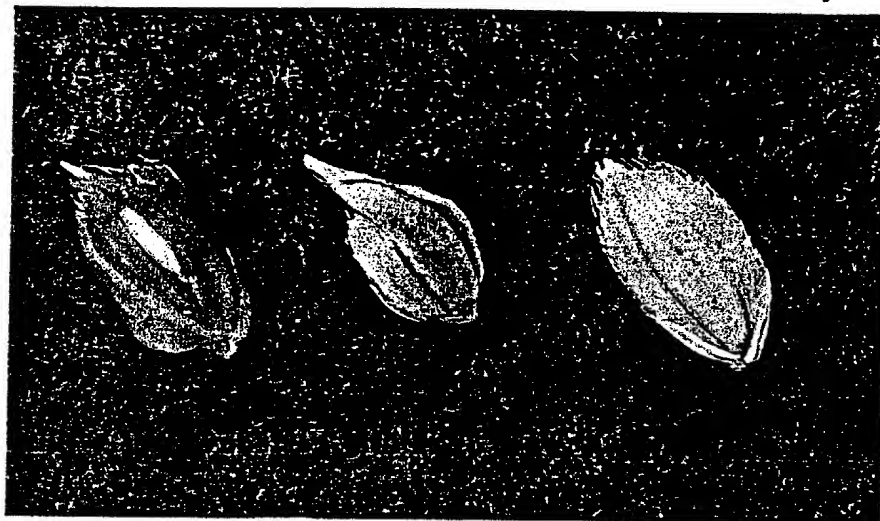


Fig. 1

A Mutant Wild Type



B Mutant Wild Type



Fig. 2

007244-1-12000

0072444.14200

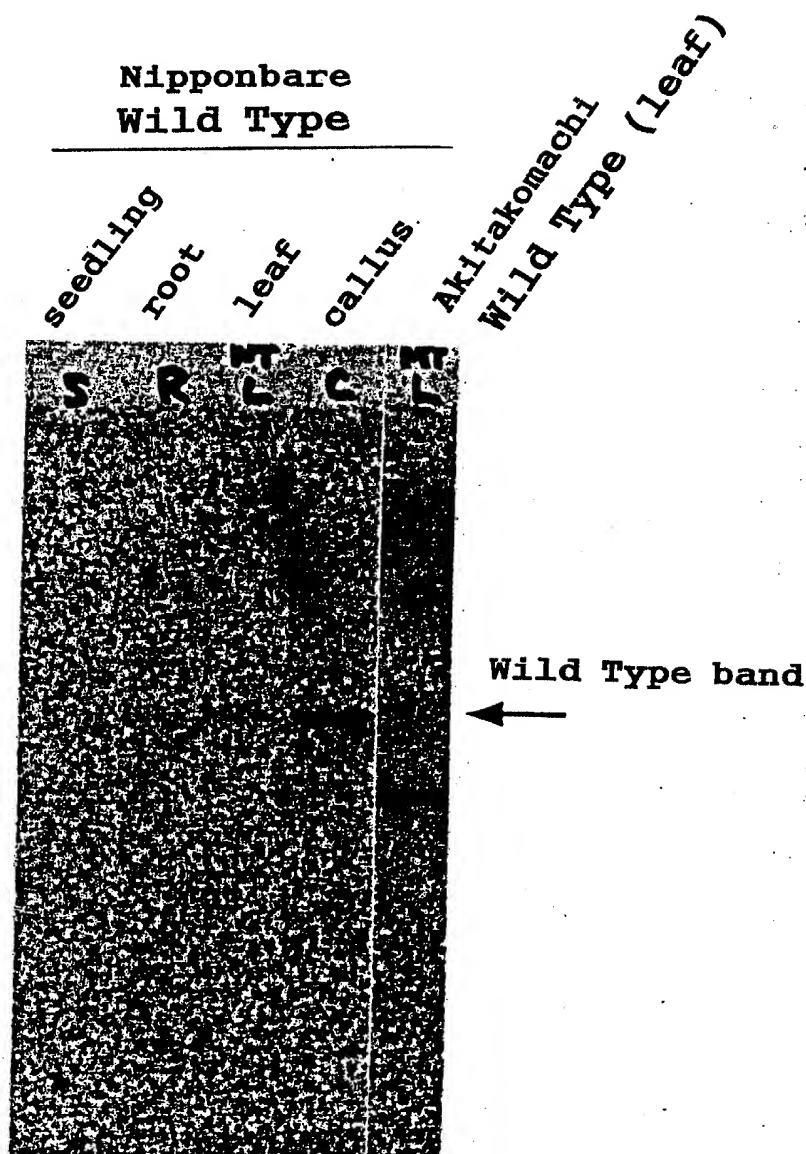


Fig. 3A

002211-1112260

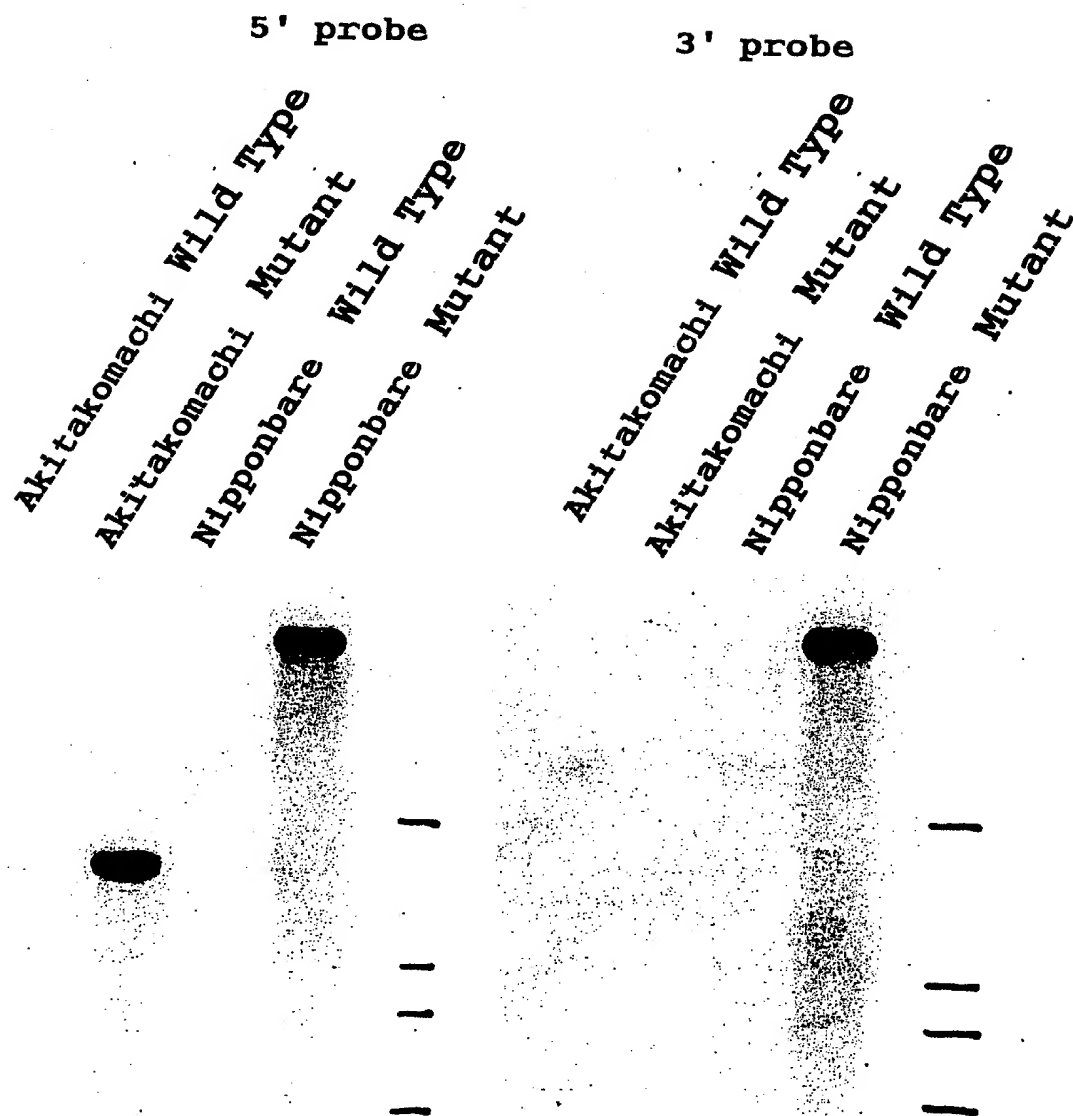


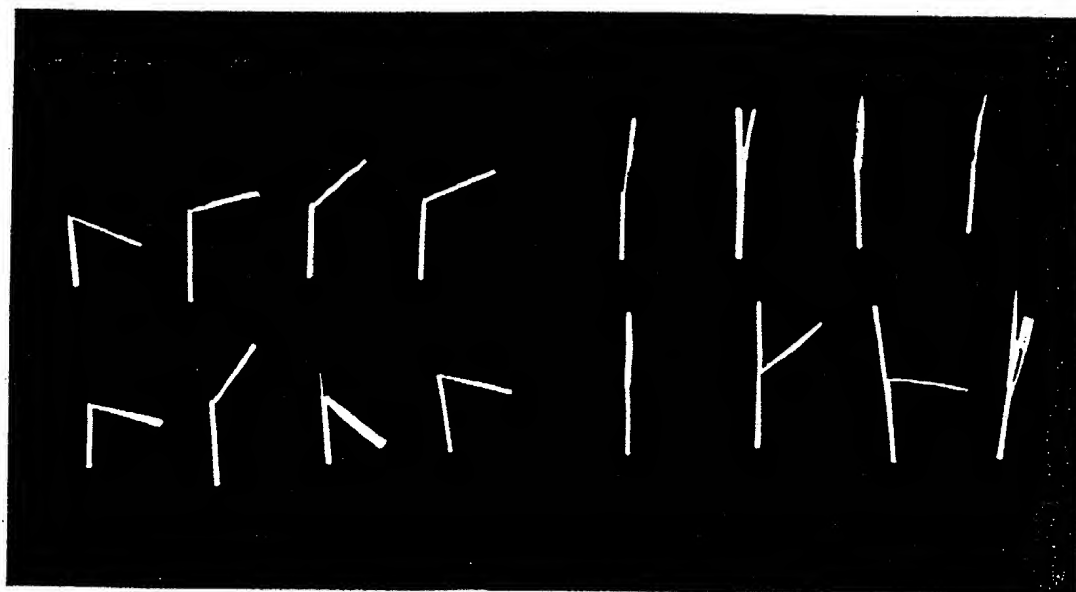
Fig. 3B

00727444500

MEIVAVDQEG ARVVGTCNML ARGGTGAVAP VLELTATPRQ DAAAEAGVDE 50
PAQHQCCEHFS IRGYVALLQK KDPKFCSLSR IFHDQKKCDE HKASSSPFSV 100
AKFRRWDCSK CLDKLKTSDN GTAPRTLPAK QNGTSDGCSI TFVRSTFVPA 150
SVGSQKVSPS TQSSQGKNAD RSTLPKSVQE GNDSKCNAPS GKNGAEEANT 200
DSPMKDLQGP AQNYDVAANV SEDNTSVDVG ALPEVPQITW HIEVNGADQP 250
PSTPKLSEVV LKRNEDENGK TEETLVAEQC NLTKDPNPMG GKERDQVAEQ 300 Nuclear localization
CNLT KDPKPV SGQKCEQICN EPCEEVVLKR SSKSKRKTDK KLMKKQOQHSK 350 signal (1)
KRTAQADVSD AKLCRRKPKK VRLLEIINA NQVEDSRSD E VHRENAADPC 400
EDDRSTIPVP MEVSMDIPVS NHTVGEDGLK SSKNKTCKKY SDVVDDGSSL 450 Nuclear localization
MNWLNKKKKR TGSVHHTVAM PAGNLSNKKV TPTASTQHDD ENDTENGLDT 500 signal (2)
NMHKTDVCQH VSEISTQRCS SKGKTAGHSK GYHSAASTK YGGESTRNGQ 550
NIHVLSAEDQ CQMETENSVL SHSAKVSPAE HDIQIMSDLH EQSLPKKKKK 600
QKLEVTREKQ TMIDDIPMDI VELLAKNQHE RQMTETDCS DINRIQSKTT 650
ADDDCVIVAA KDGS DYASSV FDTNSQQKSL ASQSTQKELQ GHLALTQES 700
PHPQNFQSTQ EQQTHLRMEE MVTIAASSPL FSHHDDQYIA EAPTEHWGRK 750
DAKKLTWEQF KATTRNSPAA TCGAQFRPGI QAVDLTSTHV MGSSSNYASR 800
QPVIAPLDRY AERAVNQVHA RNFPS TIATM EASKLCDRRN AGQVVLYPKE 850 ATP/GTP binding motif
SMPATHLLRM MDPSTLASFP NYGTSSRNQM ESQ LHSQYA HNQYKGSTST 900
SYGSNLNGKI PLTFEDLSRH QLHDLHRPLR PHPRVGVLS LLQKEIANWS 950
ENCGTQSGYK LGVSTGITSH QMNRKEHFEA LNSGMFSAKW NALQLGSVSS 1000
SADFLSARNS IAQSWTRGKG KMHVPLDRFV RQDICITNKN PADFTTISND 1050
NEYMDYR 1057

Fig. 4

Mutated line (A0369) derived from Akitakomachi

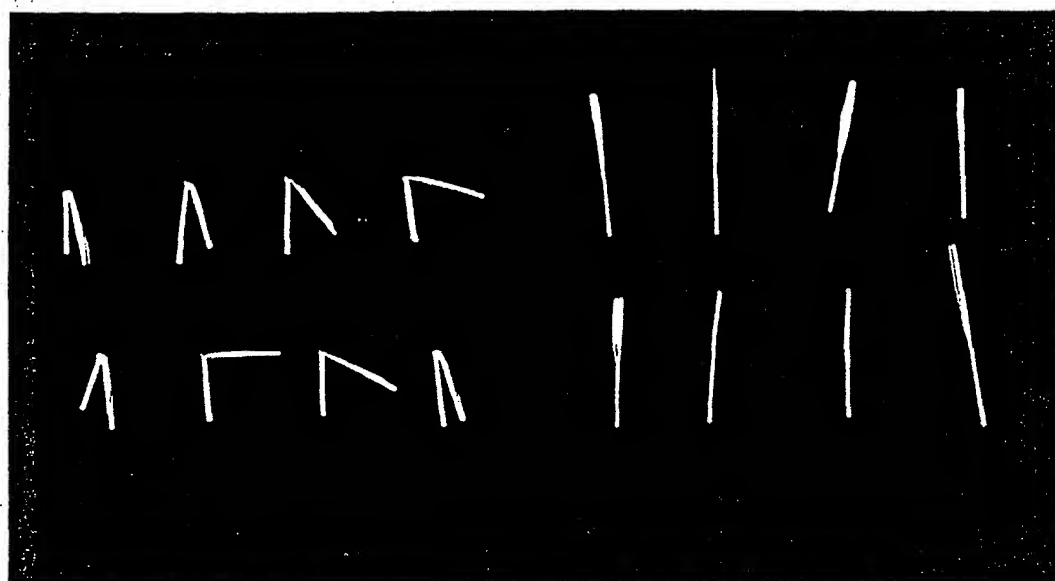


Wild Type

Mutant

Fig. 5A

Mutated line (NC6148) derived from Nipponbare



Wild Type

Mutant

Fig. 5B